

# *Cotton*



*2017 Research Accomplishments*

*USDA*

*Agricultural Research Service*

*Plains Area*

# Cotton

## NEW MEXICO

**Enhancing the Quality, Utility, Sustainability and Environmental Impact of Western and Long-Staple Cotton through Improvements in Harvesting, Processing, and Utilization**

**Southwestern Cotton Ginning Research Laboratory, Las Cruces, NM**

**Project Number:** 3050-41000-009-00-D

**Lead Scientist:** Paul Funk

**Team Members:** Robert Hardin, Albert Terrazas

**Fuel energy use patterns at cotton gins.** Fuel cost increases and consumption variability threaten gin profitability. Cotton drying systems at twenty-three U.S. cotton gins were audited during the 2017 ginning season to quantify fuel use effectiveness and identify patterns in fuel use efficiency that correlate to the various facility designs, equipment selections, or operation strategies. Fuel use efficiency was highly variable, ranging from 3 to 38 percent, and it was not possible to separate fuel use efficiency differences by specific dryer types. However, ARS researchers in Las Cruces New Mexico, were able to determine that gins with insulated drying ducts and burners located closer to the point where the heated air and cotton mixed, made better use of dryer fuel. Identifying industry best practices is a first step to recommending best practices, and an opportunity to inform wise use of resources for future research projects addressing



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fuel energy conservation. In addition, reducing fuel use improves environmental stewardship and sustainability as well as industry economic viability.

## TEXAS

### **Molecular and Genetic Approaches to Manage Cotton Diseases**

**Insect Control and Cotton Disease Research Unit, College Station, TX**

**Project Number:** 3091-22000-035-00D

**Lead Scientist:** Alois Bell

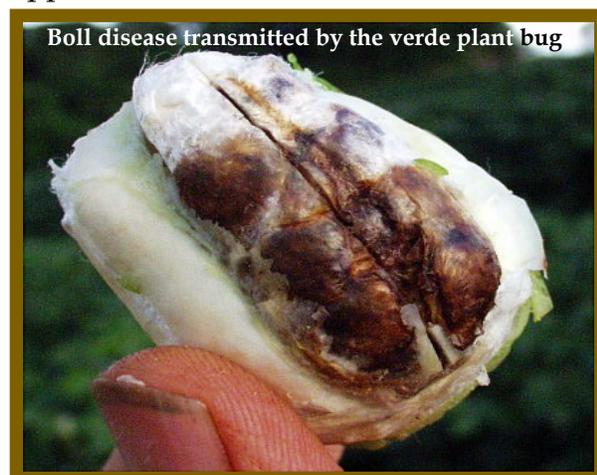
**Team Members:** Jinggao Liu, Enrique Medrano, Jesus Esquivel

#### **Association of an emerging pest of cotton with boll rot pathogen introduction.**

Beginning in 1999, significant yield losses were reported in South Carolina due to a previously unobserved seed and lint disease. The disease range expanded to include other southeastern states with yield losses as high as 15% in some fields; the disease has now reached Texas. Cotton boll fruiting structures are susceptible to infection during early developmental stages and may be infected without exhibiting external symptoms. Previously, we established that pathogenic bacterial strains are causal agents of the malady and are transmitted by piercing sucking pests such as stink bugs. In 2017, ARS researchers in College Station, Texas, in collaboration with Texas A&M AgriLife researchers, demonstrated that infestations by another sucking pest of cotton called the verde plant bug can lead to boll disease. Bolls from adjacent fields that were protected from insect attack by pesticide application were free of both insect damage and disease. The work indicates that stink



Verde plant bug on cotton



Boll disease transmitted by the verde plant bug

bugs aren't the only potential carriers of boll rot pathogens, with the capacity to transmit disease agents. The finding broadens the significance of the vector-borne disease syndrome and its effects on the bottom line of producers. Efforts to differentiate between verde bug damage due to feeding alone, and those harboring pathogens, are ongoing. Increased pesticide applications only in cases where piercing-sucking insects are carrying cotton boll pathogens, would be more effective and economical to growers than scheduled prophylactic applications.



None inoculated Pima S-7

Pima S-7 inoculated with Texas

**Detection of Fov race 4 in Texas.** *Fusarium* wilt of cotton is a widespread disease; the fungal causal agent, *Fusarium oxysporum* f. sp. *vasinfectum* (Fov), is genetically diverse. Most of the genotypes of U.S. Fov require the presence of nematodes to cause disease. Fov race 4, however, is an exception. It is extremely virulent and causes disease in the absence of nematodes, and can represent a major constraint to cotton production. In the U.S., race 4 was first reported in California in 2001 and

was confined to that state for many years. However, in June 2017, cotton plants displaying wilt symptoms from El Paso and Hudspeth Counties in Texas were tested for the presence of Fov race 4 by ARS researchers in College Station, Texas. Sixty-six Fov isolates were obtained and confirmed as race 4 by DNA sequence analysis, vegetative compatibility analysis (genetic test), a race 4 specific PCR test, and pathogenicity tests. All isolates were highly virulent on Pima S-7, killing all the plants in infested soils. Using newly developed simple PCR tests, two subpopulations of Fov race 4 were identified in Texas based on the number of transposon insertions in the PHO gene. These discoveries will be very useful in monitoring spread of Fov race 4 in the U.S. and in development of new techniques and protocols for disease control.

**Development of germplasm resistant to both nematode-requiring and nematode non-requiring Fov pathotypes in the U.S.**

Most genotypes of U.S. Fov require nematodes (vascular competent pathotype such as Fov race 1) to cause disease; and therefore they can be controlled by use of nematode resistant cultivars. However, Fov race 4 (a root rot pathotype), can cause severe wilt in the absence of nematodes; therefore, cotton host resistance to the fungus itself is needed to control the pathogen. Combining race 4 resistance with nematode resistance should generate germplasm lines resistant to both Fov pathotypes as well as nematodes. ARS researchers in College Station, Texas, have identified a near Fov4 immune line of *Gossypium arboreum* (Acc. No. 190), and its race 4 resistance was introgressed via a triple-species hybrid into Barbren 713-32 lines, that are highly resistant to both root-knot and reniform nematodes, but susceptible to Fov4. Fov4 pathogenicity assays of advanced introgressed lines showed that they also are nearly immune to race 4. Additional research is needed to evaluate these lines in Fov race 4 infested fields, as well as in Fov race 1 infested fields.



Barbren 713-32      Introgressed line      *G. arboreum* Acc. No.

**Microbial resistance mechanisms to the antibiotic and phytotoxic fusaric acid.** Fusaric acid (FA) produced by *Fusarium oxysporum* plays an important role in disease development in cotton. This non-specific toxin also has antibiotic effects on microorganisms and provides competitive advantage to the pathogen in the soil. Thus, there is likely a potential pool of diverse detoxification mechanisms in nature. In this study, ARS researchers in College Station, Texas evaluated bacteria and fungi for their ability to grow in the presence of FA and to alter the structure of FA into less toxic compounds. None of the bacterial strains were able to chemically modify FA. Highly FA-resistant strains were found only in Gram-negative bacteria. The FA resistance of Gram-negative bacteria was positively correlated with the number of predicted genes for FA efflux pumps present in the genome. In contrast, most fungi converted FA to less toxic compounds regardless of the level of FA resistance they exhibited. Five derivatives, including one unknown, were detected, and the detoxification of FA involved either oxidative reactions on the butyl side chain or reductive reactions on the carboxylic acid group. The production of these metabolites from widely different phyla indicates that resistance to FA by altering its structure is highly conserved. This information will allow cloning of the underlining detoxification genes and their incorporation into cotton or biocontrol organisms to control Fusarium wilt.

### **Conservation, Genetic Analyses, and Utilization of Cotton Genetic Resources**

**Crop Germplasm Research Unit, College Station, TX**

**Project Number:** 3091-21000-037-00D

**Lead Scientist:** Lori Hinze

**Team Members:** James Frelichowski, John Yu

**Cotton Winter Nursery (CWN) established in Costa Rica.** A counter season nursery in a tropical environment is vital to the National Cotton Germplasm Collection's (NCGC) ability to meet its mission to conserve, characterize, and distribute germplasm resources. A partnership with Cotton Incorporated has established and maintains this nursery in Liberia, Guanacaste, Costa Rica. Nearly one-third of the accessions in the NCGC are photoperiodic or slow-maturing, requiring the year round operation of this nursery. The curator and technician spend at least a week each spring working at the CWN to characterize accessions and collect data and digital images so that users can make more informed decisions when requesting accessions from the NCGC. All cotton is harvested, ginned, and acid-delinted at the



Field plots at the Costa Rica Winter Nursery

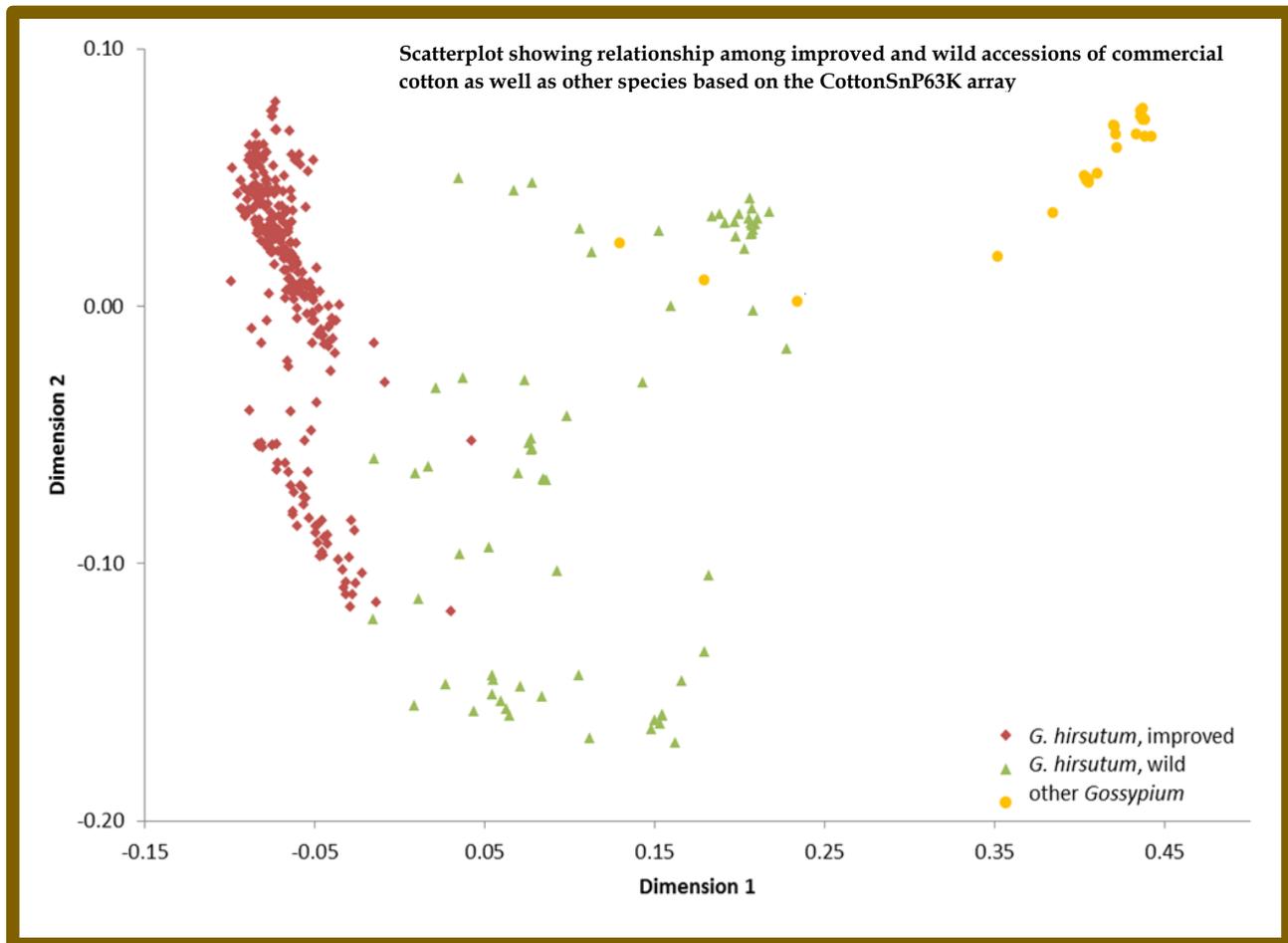


nursery so that it satisfies APHIS import and phytosanitary requirements when shipped back to the U.S. The CWN allows for seed increase of accessions that are challenging to grow and that have critically low amounts of seed. When seed is returned to the Collection, it is already delinted, thus removing a step that previously needed to be done by NCGC personnel.

This nursery is also used by cotton researchers within ARS as well as from the university community. The Costa Rican location allows researchers to accelerate their breeding programs with an additional season every year as well as make crosses with photoperiodic germplasm from the NCGC. The impact of the tropical germplasm grown in a winter nursery is exemplified by the accession GB-713 (PI 608139 'Inca Cotton'). This accession is the most requested over the past decade and continues to be used by public and private breeders to develop improved lines with nematode resistance.

**Identification of high oleic acid trait in cotton accessions.** The domestication and breeding of cotton have led to improvements in cotton yield and quality. However, the seeds have properties that give them value in secondary markets. The intense selection for elite, high fiber properties have led to reduced genetic variation of seed constituents within currently cultivated Upland cotton genotypes. Nevertheless, a recent screen of the genetically diverse National Cotton Germplasm Collection identified accessions with marked differences in seed oil and protein content. Some accessions contain commercially attractive seed oil fatty acid profiles that would improve the value of cottonseed oil, similar to other edible plant oils from soybean, corn, and canola. ARS researchers in College Station, Texas, worked with ARS researchers at New Orleans, Louisiana, and with others at the University of North Texas to discover multiple accessions of pima cotton of tropical origin that contain elevated seed oil oleic acid content. A mutation in the *FAD2-1D* gene was identified and linked to increased oleic acid seed levels. Development of markers associated with this mutation will be very useful in efforts to breed the high oleic acid trait into cultivated accessions of Upland cotton. Given the large amounts of cottonseed produced around the world that is currently not processed into higher value products, these efforts might be one avenue to raise the overall value of the cotton crop for producers.

**Molecular characterization of cotton germplasm.** Cotton and wild relatives found throughout the world contain beneficial genetic variations that traditional and genomic breeding methods can exploit to develop cultivars adapted to emerging environmental



and climate conditions. For the National Cotton Germplasm Collection, continual characterization and evaluation using the latest technologies are vital to accurately describe the resources, and allow potential users to request the most relevant accessions for cotton research and improvement. Recently, the cotton community has established a high-throughput molecular biology-based system, known as the CottonSNP63K array, which enables any researcher to simultaneously analyze large numbers of markers and obtain highly repeatable results. ARS researchers in College Station, Texas, used this Single Nucleotide Polymorphism (SNP) array to evaluate accessions from the Collection, as well as cotton cultivars submitted by researchers. The work assessed the diversity and potential of these genetic types (genotypes) for improving the cotton crop. The markers distinctly separated taxonomically defined species as well as distinguished cultivated cotton from wild and ancestral types. The markers also efficiently discerned differences among cultivars to provide other cotton researchers with a large genome-wide variation data set for cultivated cotton. Thousands of markers in representative genotypes provide an opportunity to finely discriminate among cultivated cottons to select those best suited for research programs, to avoid costly duplications of identical genotypes within germplasm collections, and to prioritize the acquisition, utilization, and maintenance of genetically diverse and distinct genotypes.

## Aerial Application Technology for Sustainable Crop Production

Aerial Application Technology Research Unit, College Station, TX

Project Number: 3091-22000-032-00D

Lead Scientist: Clint Hoffmann

Team Members: Chenghai Yang, Brad Fritz, Dan Martin

### Aerial remote sensing survey of Fusarium wilt of cotton in New Mexico and Texas.

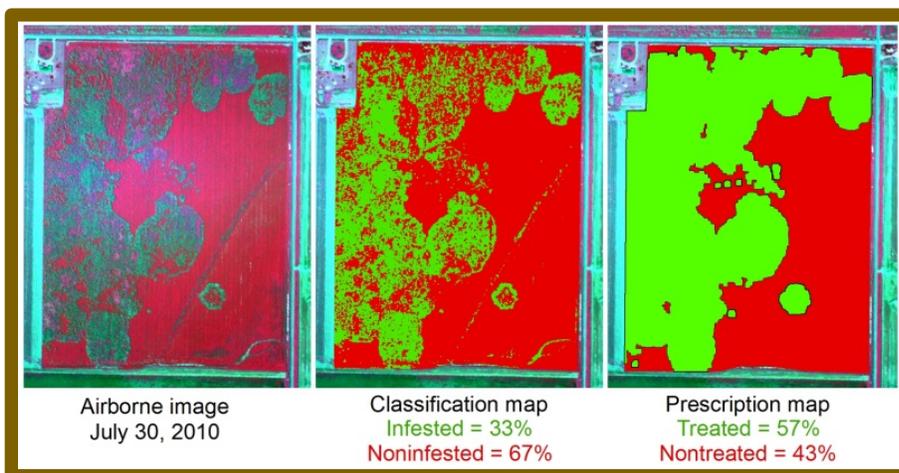


Fusarium wilt of cotton, caused by the fungus *Fusarium oxysporum* f. sp. *vasinfectum* (Fov), is a common cotton disease. Recently, the more virulent Fov race 4 (Fov4) has been identified in the New Mexico-Texas

border area near El Paso, Texas. In this study, a preliminary aerial remote sensing survey was conducted by ARS researchers in College Station, Texas, in September 2017, for mapping the distribution and severity of this emerging disease in the area. Over 600 pairs of true-color and near-infrared images were acquired from three apparently infested areas with a total acreage of about 40,000 acres near the El Paso area. Fov4-infested areas could be detected from the images for the infested fields that had been identified by ground observations and pathogen sampling. This preliminary aerial survey has provided useful information on Fov4 infestation in the New Mexico-Texas border area, but additional research is needed to evaluate different types of imagery for monitoring the progression of the disease over the season and for distinguishing it from other stresses.

### Site-specific management of cotton root rot using historical remote sensing imagery.

Cotton root rot can now be effectively controlled with Topguard Terra Fungicide, but



site-specific application of the fungicide can greatly reduce treatment cost as only portions of the field are infested with the disease. The overall goal of this 3-year project was to demonstrate how to use historical remote sensing imagery and

variable rate technology for site-specific application of the fungicide. Three years of field experiments showed that the variable rate systems performed well and site-specific fungicide treatments effectively controlled this disease with a reduction of fungicide cost by 30-60%. On the basis of the results of this multi-year research, ARS researchers in College Station, Texas developed and published a bulletin guide to provide cotton growers, crop consultants, and agricultural dealers with practical guidelines for implementing site-specific Topguard Terra application for effective management of cotton root rot.

### **Detection and Biologically Based Management of Row Crop Pests Concurrent with Boll Weevil Eradication**

**Insect Control and Cotton Disease Research Unit, College Station, TX**

**Project Number:** 3091-22000-033-00D

**Lead Scientist:** John Westbrook

**Team Members:** Jesus Esquivel, Ron Nachman, Charles Suh

**Determining refuge requirements for the cotton fleahopper in response to a new *Bt* protein for *Lygus*.** A commercial company recently developed a new line of *Bt* cotton for plant bugs. Although the new *Bt* toxin was intended for *Lygus* plant bugs, the toxin also has activity against thrips and cotton fleahoppers. Before this line can be released commercially, refuge requirements have to be established and approved by the EPA to prevent or delay the development of insect resistance to the new toxin. ARS researchers in College Station, Texas, worked with collaborators at Texas A&M University and the company to define the population dynamics and genomic structure of cotton fleahoppers in cotton fields and surrounding wild weed hosts to determine whether nearby weed patches could serve as natural refuges for the new *Bt* line. The work showed that several weed species, particularly woolly croton, provided more than adequate numbers of cotton fleahoppers to mate with cotton fleahopper populations in cotton. Additionally, our genomic data suggest mating between cotton fleahopper populations in cotton and woolly croton does occur towards the latter part of the growing season. Collectively, these findings indicate surrounding weed host patches, particularly those containing woolly croton, could serve as natural cotton fleahopper refuges for the new line of *Bt* cotton.



**Developing a pheromone lure for the southern green stink bug.** The pheromone components of the southern green stink bug have been previously reported, but the numbers, identities, quantities, or ratios of components vary among studies. Furthermore, prior pheromone formulations based on these earlier reports failed to attract stink bugs to traps in the field. Consequently, a commercially-available pheromone lure for the southern green stink bug does not exist. Through a Cooperative



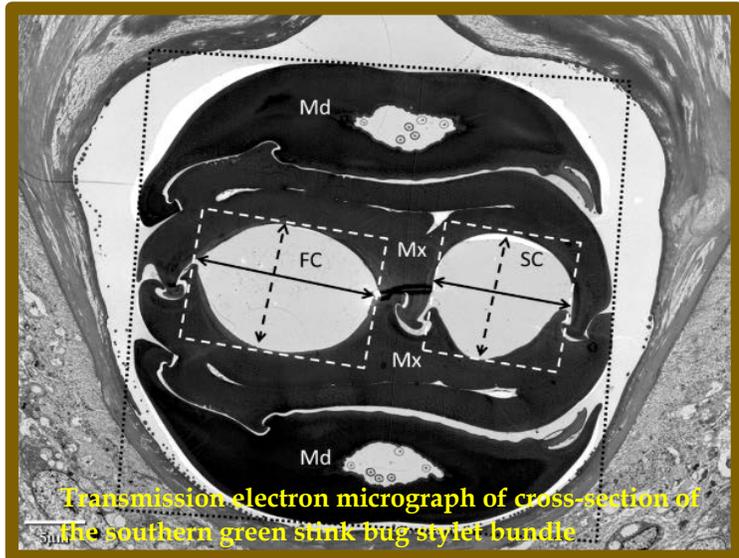
Research and Development Agreement with a commercial partner, ARS researchers in College Station, Texas, re-examined the pheromone components of the southern green stink bug and developed a new pheromone formulation. Preliminary trapping studies indicate the new formulation is attractive to southern green stink bugs, but additional trapping studies are required before the lure can be commercialized.

**Enhancing cotton plant defense with fungal endophytes.** Recent studies suggest that cotton plants colonized by certain species of fungal endophytes produce volatiles that substantially deter southern green stink bugs and *Lygus* spp. from colonizing and feeding on plants. However, it is not known whether these volatiles are produced by the fungus or if the fungus causes the plant to release the defensive compounds. ARS researchers in College Station, Texas, worked with Texas A&M University collaborators to profile the volatiles produced by cotton plants with and without fungal endophytes. Our findings indicate the profile of volatiles produced by cotton plants with and without fungal endophytes are qualitatively similar, but plants with fungal endophytes produce significantly greater quantities of  $\alpha$ -pinene, limonene, and humulene. The greater emission of limonene suggests the fungal endophytes are affecting the jasmonate and ethylene pathways in cotton plants, which already have been shown to play a critical role in plant defense against insect herbivores. Studies are currently underway to determine the mechanisms by which these fungal endophytes activate the defensive response genes in cotton.



**Morphology and internal dimensions of the southern green stink bug feeding apparatus.** Southern green stink bugs transmit disease-causing pathogens of cotton.

Adults were recently shown to ingest multiple types of pathogens, but only select pathogens were transmitted. Consequently, it was hypothesized that the food canal within the feeding apparatus (i.e., a stylet bundle composed of modified mouthparts that form the salivary canal and food canal) may affect ingestion and transmission of pathogens. ARS researchers in College Station, Texas, sectioned the head and labium, which house the stylet

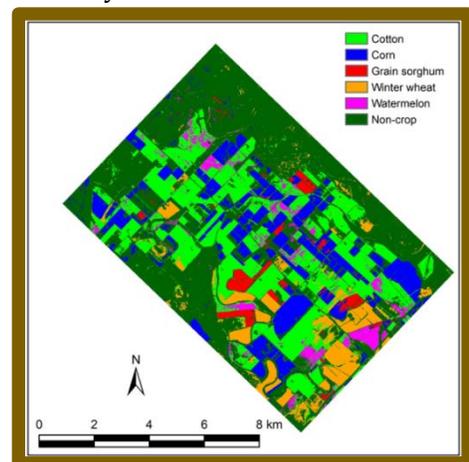


Transmission electron micrograph of cross-section of the southern green stink bug stylet bundle.

bundle of southern green stink bug adults, and established the internal dimensions of the canals at both locations. The food and salivary canals were shown to differ in shape; the food canal being more ellipsoid versus the more circular salivary canal. Food and salivary canals were shown to be larger at the labium than within the head, thereby producing a 'funnel' effect towards the head. Both observations of differing canal shapes and variation in dimensions along the respective lengths were previously unknown. Overall, food canals were found to be sufficiently large to allow ingestion and transmission of all disease-causing pathogens previously examined; this observation suggests other biotic factors affect transmission of ingested pathogens.

**Using multispectral satellite imagery to identify cotton fields.** Timely knowledge of the location of all cotton fields is critical to the success of boll weevil eradication programs in the U.S. Historically, eradication programs relied on data compiled by the Farm Service Agency to locate cotton fields, but this information may not be available until the end of the growing season. Consequently, fields

infested with weevils may not be monitored with pheromone traps or treated with insecticides throughout much of the growing season. ARS researchers in College Station, Texas, including a scientist from in-house project 3091-22000-032-00D, developed a technique to analyze multispectral satellite images to accurately identify cotton fields during the early- to mid-growing season. This technique is currently being evaluated by the Texas Boll Weevil Eradication Foundation to accurately



identify the position of all cotton fields in the Lower Rio Grande Valley and Winter Garden production areas of Texas.

**Using population genomics to identify geographical sources of boll weevil re-infestations.** The boll weevil has been eradicated from >92% of the cotton acreage in the U.S., but economic infestations still remain in the southern portions of Texas. These remaining weevil populations as well as those in the Mexican states of Tamaulipas, Coahuila, Durango, and Sonora, continue to pose a threat as sources of weevil re-infestations. If an area in the U.S. is re-infested with boll weevils, proper mitigation and development of remedial actions will require accurate identification of the geographical origin of the re-infestation. ARS researchers in College Station, Texas, worked with Texas



A&M University and USDA-APHIS colleagues to define aspects of the genomic structure of weevil populations collected from the aforementioned geographical areas. The work established that each geographical population of weevils possessed unique genetic markers, which can be used to distinguish the respective weevil populations. Efforts are currently underway to analyze the genomic structure of boll weevil populations from various cotton production areas in Central and South America.

## Developing Genomic and Genetic Tools for Exploiting Cotton Genetic Variation

Crop Germplasm Research Unit, College Station, TX

Project Number: 3091-21000-038-00D

Lead Scientist: John Yu

Team Members: Lori Hinze, James Frelichowski

**CottonGen: A database resource for the cotton genomics, genetics, and breeding research community.** Rapid

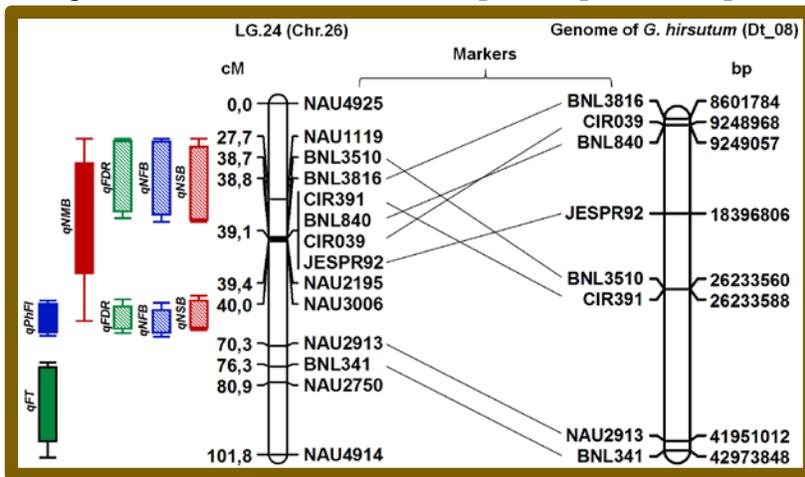
advances in high-throughput genomic and phenomic technologies have led to an explosion of research data for cotton. A well-developed and managed database with bioinformatic tools is essential to provide cotton researchers and producers with critical datasets and bioinformatic resources to analyze



The screenshot displays the CottonGen website interface. At the top, there is a navigation menu with links for Species, Data, Search, Tools, ICGI, and General, along with a search bar and a login button. The main content area features the CottonGen logo and the text 'COTTONGEN COTTON DATABASE RESOURCES Genomic, Genetic and Breeding Resources for Cotton Research Discovery and Crop Improvement'. Below this, there are sections for 'News and Events' with a list of recent updates, 'Major Species Quick Start' with icons for arboreum, barbadense, herbaceum, and hirsutum, and 'Tools Quick Start' with a grid of tool categories including genomics, genetics, breeding, and general. The footer contains logos for various partner organizations like Cotton Incorporated, USDA, Bayer CropScience, DOW, and NRSPIO.

them. ARS researchers in College Station, Texas, worked with cooperators at Cotton Incorporated, Washington State University, and others in the cotton research community to develop a central data repository called CottonGen (<https://www.cottongen.org/>) that merged several previous cotton databases including CottonDB. Using open-source Tripal database infrastructure, CottonGen serves as an informatics resource for cotton researchers, facilitating research discovery and cultivar improvement by providing a genomics, genetics, and breeding database. In addition to vast data curation, CottonGen has integrated analysis and visualization tools such as JBrowse and GBrowse, BLAST+, CottonCyc, MapViewer and CMap. CottonGen recently released a Cotton Trait Ontology, CottonGen Reference Transcriptomes (RefTrans), and will soon release the Breeders Information Management System (BIMS). As the home of the International Cotton Genome Initiative (ICGI), CottonGen continues to support the worldwide cotton research community by providing useful research data and bioinformatic tools. Over the past year, CottonGen has been accessed more than 100,000 times by many thousands of cotton researchers, breeders, and others from more than 100 nations.

**Genetic parameters associated with flowering-time and photoperiod insensitivity of *Gossypium darwinii* Watt.** While most wild and semi-wild *Gossypium* species are photoperiod-sensitive, they provide a valuable source of genes for genetic improvement of modern cotton cultivars. ARS researchers in College Station, Texas, worked with cooperators at the Uzbekistan Academy of Sciences and other ARS researchers at Mississippi State, Mississippi, and Lubbock, Texas, to construct genetic linkage maps using DNA markers called Simple Sequence Repeat (SSR), and Cleaved Amplified



Comparison of mapped QTL markers of *G. darwinii* (left) with actual genomic positions of *G. hirsutum* (right). Colored bars to the left indicate the relative position of trait-linked QTLs.

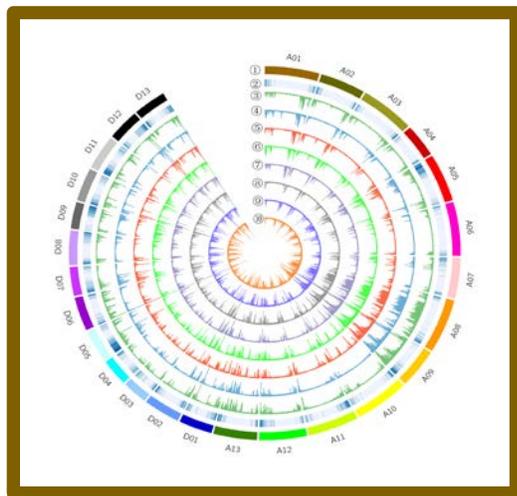
flowering-time and photoperiodic flowering. These traits segregated in an F<sub>2</sub> population grown under long day and short night summer conditions. In addition, eight QTLs were discovered in an F<sub>3</sub> population of the same cross. Two QTLs were common in both populations. Annotations of the flanking DNA sequences of mapped SSR markers from the sequenced cotton (*G. hirsutum*) genome database identified several potential genes

Polymorphic Sequence (CAPS). These maps were constructed from a biparental cotton population segregating for photoperiodic flowering in a cross between a photoperiod insensitive irradiation mutant line and its pre-mutagenesis photoperiodic wild-type *G. darwinii* Watt genotype. On the maps, six genetic parameters called

Quantitative Trait Locus (QTL) were discovered with direct association of

known to be associated with regulation of flowering characteristics of plants. The outcome of this work extends our understanding of the genetic and molecular mechanisms of photoperiodic flowering. Identified markers are useful for marker-assisted selection in cotton breeding to improve early flowering characteristics.

**Genome-wide genetic variation among eight Upland cottons.** Although efforts have been undertaken to exploit genetic variation for yield and quality improvements, limited



progress has been made in using beneficial alleles in domesticated and undomesticated varieties in cotton breeding. Building upon our previous accomplishments with the Upland cotton genetic standard TM-1, whose reference genome was released to the cotton research community, ARS

Upland cotton (*G. hirsutum*) has 26 chromosomes (A01-13) and (D01-13) (outermost circle). Gene density (second outer circle) is displayed on each of 26 chromosomes (A01-D13) and each of 8 cotton cultivars (circles 3-10). Colored peaks represent the intensity of cotton genome-wide variation.

researchers in College Station, Texas, worked with cooperators at the Chinese Academy of Agricultural Sciences to conduct extensive studies

to capture genetic variation among eight Upland cottons of direct relevance to cotton improvement. More than 3 million genetic tools known as Single Nucleotide Polymorphism (SNP) markers were developed. Genome sequence and transcriptome analysis of a widely cultivated Upland cotton, CRI-12, and its parental and progeny cultivars, revealed that 118, 126, and 176 genes with increased expression correlated with resistance to *Verticillium dahliae* (a soil fungus causing wilt disease of cotton), to salinity, and to drought, respectively. The genetic variation also included genomic loci that may have been subject to artificial selection and documented the haplotype inheritance and recombination, shedding light on the genetic mechanism of artificial selection and guiding breeding efforts for the genetic improvement of cotton.

## **Enhancing the Profitability and Sustainability of Upland Cotton, Cottonseed, and Agricultural Byproducts through Improvements in Pre- and Post-Harvest Processing**

**Cotton Production and Processing Research Unit, Lubbock, TX**

**Project Number:** 3096-21410-008-00-D

**Lead Scientist:** John Wanjura

**Team Members:** Gregory Holt, Mathew Pelletier

**Onboard cotton harvester system for weighing and calibrating yield monitor.** A novel system for measuring cotton weight onboard commercial cotton harvesters was developed and successfully tested by ARS researchers in Lubbock, Texas. The system uses hydraulic pressure measured in the harvester basket lift cylinder circuit along with



a specially developed algorithm to calculate the weight of cotton in the harvester basket. Plot average seed cotton yield is calculated from the hydraulic weight measurement and area harvested measured by an integral GPS system. The system provides essential weight data for producers or researchers seeking to calibrate cotton yield monitors, and it can be used as a stand-alone tool to conduct on-farm research in which total plot seed cotton yield is the evaluation metric. This system costs about \$5,000 to build and install, saving producers or researchers on the order of \$45,000 for a mobile scale system typically used to provide seed cotton weight measurements. Through the development of this system, producers now have access to low-cost, reliable cotton weight data on a real-time basis which will help them adopt site specific management practices which can save thousands of dollars each year in reduced input costs.

**Agricultural by-products replace fossil-fuel based acoustic absorbers for noise suppression.** There is a need to utilize agricultural by-products while minimizing fossil-fuel materials in an effort to become more sustainable. ARS researchers in Lubbock, Texas, examined the use of a novel renewable resource in acoustic absorption applications. The material is an all-natural biopolymer that consists of a combination of processed agricultural by-products and fungal mycelium. This new biopolymer provides an alternative to Styrofoam, closed cell foams and synthetic honeycombs. The study found that these new panels exhibit superior acoustical absorption properties; in comparison to traditional acoustic ceiling panels constructed from fossil-fuel based synthetic fibers and unhealthy formaldehyde glues. The results of the study indicate these mycelium panels are a promising bio-based all-natural fiber alternative for acoustic

shielding products, which can provide a sustainable alternative to traditional acoustic absorbers.

**Low-cost acoustic method provides increased accuracy.** Accepted acoustic testing instruments are available; however, they cost in excess of \$25,000, as they require specialized hardware and software that are typically out of reach economically to the occasional practitioner. What is needed is a simple and inexpensive screening method that can provide a quick comparison for rapid identification of the most promising samples to be tested. ARS researchers in Lubbock, Texas, during the evaluation of a new sustainable all-natural agricultural acoustic panel derived from cotton by-products and fungi, have developed a novel low-cost acoustic test method that can be built for under \$2,500. The new method reduces the number of required microphones to a single microphone and removes the need for simultaneous capture and extensive signal-processing analysis. In addition to the dramatic 10:1 reduction in cost of the instrument, the study discovered several unique accuracy advantages of this new method in comparison to the existing standard methods. The proposed new method provides an easy-to-use technique that requires little in the way of equipment and can be set up with minimal training and expense.

### **Enhancing Plant Resistance to Water-Deficit and Thermal Stresses in Economically Important Crops**

**Plant Stress and Germplasm Development Research Unit, Lubbock, TX**

**Project Number:** 3096-21000-019-00-D

**Lead Scientist:** Paxton Payton

**Team Members:** Mauricio Ulloa, Zhanguo Xin, John Burke, Yves Emendack, Junping Chen, James Mahan

**Alternative genetic source for improving fiber quality of cotton.** Cotton produces the most important natural fiber worldwide. Moreover, the quality of this fiber is a key factor for determining end-gain for producers, and price and quality of cotton textile products. As yield, fiber quality is significantly affected by different environmental factors/stress conditions, and genetic improvement can be a challenge due to the narrow genetic base of modern cotton cultivars. ARS researchers in Lubbock, Texas, and Cotton Incorporated announced the joint release of seven Upland cotton germplasm lines that possess competitive lint yield, superior fiber



strength, length, and uniformity when grown on the High Plains of Texas. The lines can be used as parental sources for improving fiber quality traits, such as, fiber strength, length, and uniformity under reduced irrigation levels. For public and private breeders, PSLC-U01-U07 germplasm lines provide an alternative source for improving fiber quality of High Plains' cotton because of their good yield, and superior and stable fiber properties under different irrigation conditions.

**Improved Pima cotton germplasm lines (Pima SJ-FR05 – Pima SJ-FR09) with resistance to Fusarium wilt race 4 (FOV4) and good lint yield and fiber quality.** Cotton breeders continue to need alternative sources of cotton breeding lines for improving Fusarium wilt (FOV race 4) resistance in Pima cotton in California. FOV race 4 is a fungus that has affected cotton yields in the San Joaquin Valley (SJV) for the last 12 years and in 2017



reported for the first time in west Texas. For this purpose, the Agricultural Research Service, United States Department of Agriculture and University of California announced the release of five Pima cotton germplasm lines: Pima SJ-FR05, Pima SJ-FR06, Pima SJ-FR07, Pima SJ-FR08, and Pima SJ-FR09. These lines possess good resistance to FOV race 4, and good lint yield and fiber quality characteristics such as fiber fineness, length, and strength. Pima

SJ-FR05-FR09 series originated from the cross of germplasm lines, Pima S-6 and 89590. Pima-S6 possesses a major gene(s) for FOV race 4 resistance. The SJ-FR05-FR09 lines showed good resistance to FOV race 4, compared to the resistant and susceptible checks, and parental lines. In addition, field experimental data revealed that the Pima SJ-FR05-FR09 series showed good fiber quality traits (length, strength, and fineness) when compared to the SJV Pima cotton standard of California. The SJ-FR05-FR09 series are helping to speed efforts to broaden the genetic base, which is critical to the success and future of the Pima cotton industry. These lines are being used by a seed company in California.

**Analysis of root-knot nematode and fusarium wilt disease resistance in cotton (*Gossypium* spp.) using chromosome substitution lines from two alien species.**

Diseases caused by nematodes, such as root-knot nematode (RKN), and caused by fungi such as Fusarium (FOV races 1 and 4), represent expanding threats to cotton production. Resistant cultivars are highly effective in preventing crop loss from RKN and FOV infection, economically important diseases in cotton. To identify a new resource of cotton types resistant to these two pests and favorable genes associated with nematode and fungal disease resistance traits, ARS researchers in Lubbock, Texas, used a series of cotton chromosome substitution (CS) lines in this study. RKN and FOV greenhouse and infested

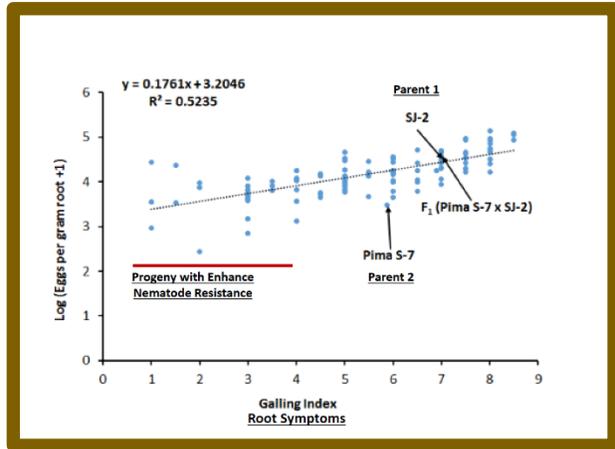
field evaluations identified CS lines with improved resistance. CS lines carrying small alien chromosome segments with favorable gene-alleles could be used for effective introgression of stress and disease resistance or many other desirable traits by targeting gene interactions and reducing barrier effects. Molecular marker analyses validated regions on cotton chromosomes 11, 16, and 17 harboring RKN, FOV race 1, and FOV race 4 resistance genes, respectively. Also, analyses from this study demonstrated the value of these cotton CS lines as a germplasm resource for breeding programs.



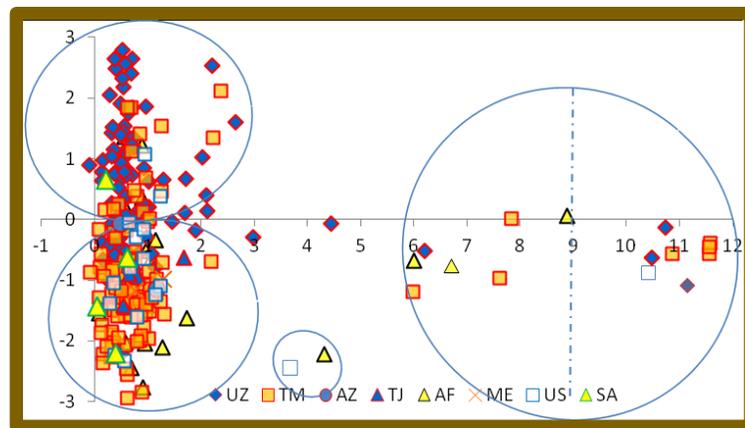
**Mapping of multiple independent genes-loci for resistance to fusarium wilt races 1 and race 4 in cotton population progeny or lines.** The soil-borne fungal pathogen *Fusarium oxysporum* f. sp. *vasinfectum* (FOV), caused one of the most devastating vascular diseases in many cash crops, especially in cotton. Fusarium types represent expanding threats to cotton production in the U.S. and in other countries of the world. Resistant cultivars are highly effective in preventing crop loss from FOV infection. Progeny and breeding lines developed between Pima and Upland cottons were used by ARS researchers in Lubbock, Texas, to identify molecular markers associated with FOV race 1 (FOV1) and race 4 (FOV4) resistance. Analyses from this research validated the importance of previously reported markers and chromosome regions (c8, c14, c16 and c17 for FOV resistance) based on disease plant-symptoms and added new information for the location of FOV1 resistance genes (c12). In these cotton progeny or lines, both parents contributed resistance to FOV1 and/or FOV4. In addition, QTL analyses of these cotton lines revealed separate multiple loci determining resistance to FOV1 and FOV4, confirming that race specificity occurs in *F. oxysporum* f. sp. *vasinfectum*. Some of the breeding lines showed resistance to both fusarium wilt types, providing multiple resistance sources for breeding. These new trait-linked markers provide a valuable resource for marker assisted selection or MAS of FOV resistance during the breeding process.

**Analysis of enhanced or transgressive nematode resistance in tetraploid cotton reveals complex interactions in chromosome 11 regions.** Worms or nematodes such as root-knot nematode (RKN) caused disease in plants and represent constant threats to cotton production. Developing RKN resistant cultivars is an important breeding approach, and developed cultivars are highly effective in preventing crop yield loss from RKN infection. In this study, ARS researchers in Lubbock, Texas, investigated how RKN resistance is increased on progeny or breeding lines using different cultivars as parents in multiple-crosses. This enhancement on resistance is also known as transgressive resistance. Transgressive resistance to RKN was found in Upland cotton populations, *Gossypium*

*hirsutum* resistant NemX x susceptible SJ-2, and Pima by Upland [*G. barbadense* (susceptible Pima S-7) x *G. hirsutum* (NemX)] cotton populations. Analyses revealed contributions to RKN infection-resistance associated with a molecular marker (SSR) CIR316 linked to resistance gene *rkn1* in NemX on Chromosome 11 in seven populations. In addition, markers closely linked to SSR CIR316 contributed up to 82 percent of resistance to infection (root-galling). Stronger transgressive resistance occurred in later, rather than in early generations in the Upland-by-Upland crosses, than in the Pima by Upland crosses. Transgressive effect on progeny from susceptible parents is possibly provided on the *rkn1* resistance region of chromosome 11 by tandemly arrayed allele (TAA) or gene (TAG) interactions contributing to transgressive resistance. Complex TAA and TAG recombination and interactions in the *rkn1* resistance region provide a model to study disease and transgressive resistance in complex-polyploid plants, and novel cotton-genotypes for plant breeding.



### Genetic diversity, linkage disequilibrium, and association mapping analyses of *Gossypium barbadense* L. cotton germplasm and cultivars.



Principal component analysis, of 288 *G. barbadense* cultivars in the space of two main coordinate jointly by SSR genotypes. PC - the main components; A and B - 1 genetic subpopulation subgroup represented in the majority of cultivars of Uzbekistan and Turkmenistan, respectively. Small circle marked genetically isolated African accessions belonging to subgroup B. big circle isolated subpopulation 2, represented by the most genetically differentiated samples. UZ - Uzbekistan, TM - Turkmenistan, TJ - Tajikistan, AF - Africa, US - USA, SA - South America AZ -Azerbaijan and ME -Middle East.

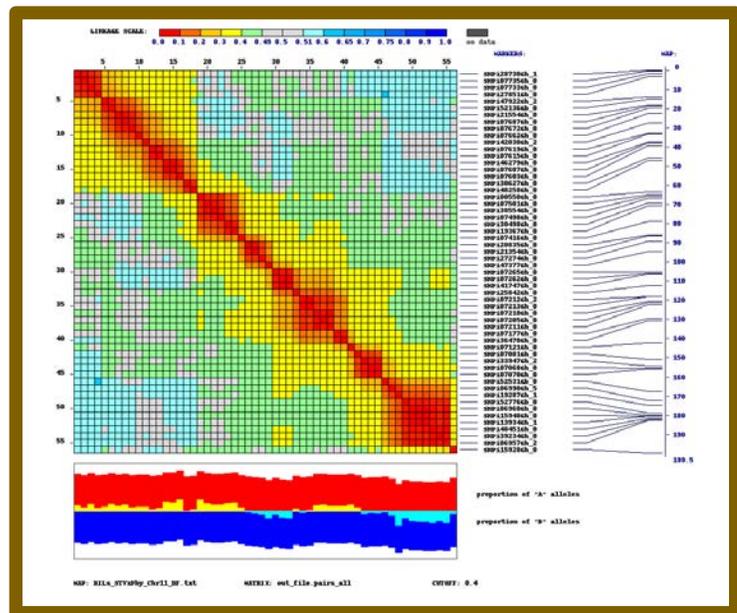
Cultivated cotton is the most important natural fiber worldwide. Fiber quality is a key factor for determining price and quality of cotton textile products. Genetic improvement of fiber quality is a challenge due to the narrow genetic base of modern cotton cultivars and the effect of the environment on fiber quality. The narrow genetic base is due to the use of a few elite cotton lines to develop progeny also known as a genetic bottleneck through historic domestication. This narrow genetic base and the breeding challenges of cotton highlight a great need to study genetic resources preserved and maintained in world cotton

germplasm collections, and the use of these resources in breeding of superior cotton cultivars. In this study, 288 worldwide *Gossypium barbadense* L., also known as Sea Island,

Egyptian, or extra-long staple (ELS), or Pima cotton germplasm and cultivars were evaluated by ARS researchers in Lubbock, Texas, in two diverse environments, Uzbekistan and the USA. In addition, this is the first SSR marker-based molecular genetic study conducted of *G. barbadense* cotton germplasm from the Uzbekistan cotton collection. Molecular and fiber trait (strength, length, etc.) analyses in the two diverse environments provide insights into the breeding history and genetic relationship of *G. barbadense* germplasm and cultivars. Molecular markers were associated with fiber quality traits and these markers were found to be consistent with previous fiber trait-associations. In addition, based on this genetic diversity study, it can be hypothesized that the formation of the accessions of this studied *G. barbadense* collection was formed by the introduction/introgression of African (including Egyptian), African-American and American genotypes. It is also important to notice that as a result of many years of breeding, the population of *G. barbadense* cultivars formed gene pools and/or genotypes specific to agro-ecological conditions of the Central Asian region, and clearly traced the genetic isolation of the Uzbek and Turkmen cultivars. Results from this study should also be helpful for improvement of cotton cultivars using a molecular breeding approach.

**Insights into upland cotton (*Gossypium hirsutum* L.) genetic recombination raised on 3 high-density single-nucleotide polymorphism and a consensus map developed independently with common parents.**

Cotton is the most important renewable natural textile fiber worldwide. In the last decade, considerable progress has been made towards the development of new cotton tools and genomic resources. However, genomic resources in cotton are still behind, compared with other crops such as maize, sorghum, rice, soybeans, etc. With the availability of a new technology to sequence DNA, or blueprints/genes called next generation sequencing, additional resources and platforms are being developed, and larger number of molecular markers such as single nucleotide polymorphism (SNP) are being identified in the cotton crop for assisting breeding. In this study, three high-density genetic linkage SNP maps and a consensus map or joinmap using the CottonSNP63K array were developed from three independently developed intra-specific Upland cotton populations by ARS researchers in Lubbock, Texas. Molecular linkage maps based upon DNA markers serve as the backbone for genetic analyses and are widely recognized as an

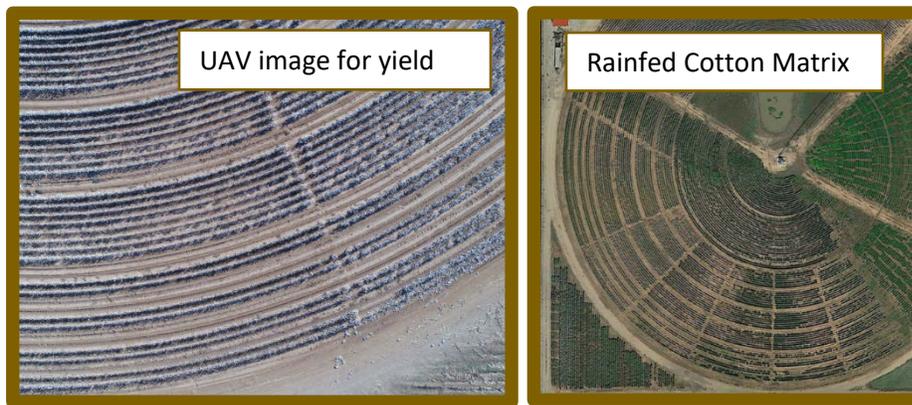


Cotton Chromosome 11 from Stoneville 474 x Phytogen 72 RIL mapping population

essential tool for genetic research in many crops. In addition, maps provide an excellent framework for discovering loci and/or genes responsible for traits of interest. This is the first intraspecific SNP genetic linkage joinmap assembled in Upland cotton with a core of reproducible SNP markers assayed on different populations, and it provides further knowledge on the order and arrangement of genes, chromosome arrangements, and relationships of progeny vs parents. Together, the consensus map and cotton populations provide a synergistically useful platform for expedited localization and identification of genes and agronomically important genes for improvement of the cotton crop.

### **Elucidating genotype-by-environment interactions that impact cotton fiber quality.**

The second year of a rainfed research study was completed. A total of 40 pairs of rain:environment:yield relationships have been generated for 2 commercial varieties. Data is being analyzed and a manuscript is in preparation. A method for cotton yield measurement using an unmanned aerial vehicle (a drone) was developed with a result of 85% agreement between the UAV and hand harvested data. The method compares well with machine harvest results as well. In conjunction with Australian collaborators from CSIRO, ARS researchers in Lubbock, Texas, analyzed the appropriateness of historic heat



UAV-based aerial image for cotton crop development and yield measurement.

unit methods for prediction of cotton development in modern varieties and management systems. This work established that the 15° C-based heat units used in the Lubbock region are generally still sufficient while the 12°C-based heat

units commonly used in Australia might be improved. The inclusion of a 35°C high temperature cut-off may improve predictive ability to some extent.

### **Comparison of hydrocarbon yields in cotton from field grown vs. greenhouse grown.**

The interest in sustainable and renewable sources of petrochemicals continues from arid and semi-arid land crops because of the uncertainty of sustained crude oil production in the world. Recently, ARS researchers in Lubbock, Texas, reported that cotton presents a new possibility as a hydrocarbon source because of its growth habit as a perennial crop and adaptation to long and hot growing seasons. To further investigate hydrocarbon (HC) production in cotton, four cultivars (SA-1181, 1403, 1419, and 2269) from the USDA National Cotton Germplasm Collection were grown both in field conditions and a greenhouse to compare the environmental effects on leaf biomass, percent-yield of HC,

and total HC (g HC /g leaves) under natural and controlled (protected) conditions. In addition, the HC production was also investigated through different developmental stages under these different conditions. Overall, the environmental component to the yield of free HC in cotton leaves was a major factor. All four cultivars produced high percent-HC yields under field conditions. This trend corresponds to literature reports of large induction of defense chemicals in cotton upon attack by herbivores and diseases. The same pattern has been found in sunflowers and is discussed in regards to cotton in this report. Through the different developmental stages, the variation in HC for cultivar SA-2269 showed that HC yields in leaves remained at a constant, low level from bud to flowering, and then increased rapidly as bolls matured. In addition to its valuable fiber and seed for oil, cotton could also be another possible renewable source for hydrocarbons, and promising accessions in the USDA Germplasm Collection are readily available to all breeders and scientists.